RECEIVED
CENTRAL FAX CENTER
FEB 22 2007

REMARKS

In view of the following remarks, the Examiner is requested to allow Claims 1-10 and 12-16, the only claims under examination in this application.

Claims 1-3, 5-7 and 12-14 have been amended solely to clarify the claim language. Accordingly, no new matter has been added.

The Amendments should present no new issues for the Examiner.

As no new matter has been added by way of these amendments, the entry thereof is respectfully requested.

Claim Rejections – 35 U.S.C. § 102

Claims 1-10 and 12-16 remain rejected under 35 U.S.C. § 102(b) as allegedly being anticipated by Albitar et al. (Molecular Diagnosis, 1997).

The rejected claims are directed to a method of producing a biopolymeric array. The method includes immobilizing a population of a number of copies of a probe for a target to a surface of a solid support. An element of the method is that the number of copies of probes of the population is dependant on the anticipated abundance of the target in a sample.

According to the Applicants' specification, in certain embodiments of the disclosed invention, it is desirable to obtain information related to the abundance of a target suspected of being present in a sample. In order to determine this, the Applicants have developed a method of producing an array that takes the expected abundance of a target molecule in a sample into account in the design of the array. Hence, a given probe population may be designed with respect to the probe copy number so as to provide a particular signal level that relates to the abundance of a specific target in the sample. Therefore, the design of the array can be adjusted to

account for circumstances where there would typically be a low signal to high noise ratio, by making the number of a population of probes dependent on the anticipated abundance of target in the sample and thereby, in certain embodiments, boosting the signal to noise ratio. See paragraph 87.

The Office asserts that Albitar teaches this method and points to page 172, column 2, in support of this assertion. Specifically, the Office states that "Albitar places the probes in anticipation of the abundance of target." The Applicants respectfully disagree and contend that Albitar does not teach a method wherein the number of a population of probes is dependant on the anticipated abundance of target in a sample.

What Albitar actually teaches at page 172, column 2, is the following:

Simplified PCR9 Assay

Previous reports have suggested that oligonucleotides with longer dT tails were more efficiently fixed to nylon membrane [21]. Using nitrocellulose membrane, we tested the efficiency of using 20-base oligonucleotides without dT tails. As shown in Figure 1, on hybridization to a ^{32}P-end-labeled PCR product, an adequate signal can be detected on overnight exposure using 15 pmol of the oligonucleotide. This signal appears linear with the amount of oligonucleotide attached to the membrane, as shown using 15, 75, and 375 pmol. Mutant and wild-type oligonucleotides for codons 12 and 13 were blotted on one strip, and those for codon 61 were blotted on a separate strip (Fig. 2) for each of the N-*ras*, H-*ras*, and K-*ras* oncogenes, yielding six total strips.

As can be seen with reference to the above passage, although Albitar discloses that 15, 75 and 375 pmols of oligonucleotide probes are attached to a nylon membrane, there is no teaching within Albitar that these amounts are in any way related to the expected abundance of target in the sample. Rather, with respect to the sample, Albitar simply discloses that:

Peripheral blood samples from 3 normal individuals, bone marrow samples from 2 normal individuals, and bone marrow samples from 16 patients with CMML were tested for *ras* gene mutations. Figure 2 shows representative samples of RDB assays showing mutations. Four cell lines (HS578, MDA-MB231, PA1, and HL60) with known *ras* mutations were used as positive controls and showed the expected mutations: A→T in codon 61 of N-*ras* in HL60, G→A in codon 12 of H-*ras* in HS578T, G→A in codon 13 of K-*ras* in MB231, and G→A in codon 12 of N-*ras* in PA1 (data not shown). No mutation was detected in any of the samples from normal individuals. Five mutations were detected in the 16 (31%) samples from CMML patients (Table 1). The mutations were in the N- and K-*ras* oncogenes. No mutations were detected in the H-*ras* oncogene.

Contrary to the assertion of the Office, at no point in time does Albitar teach that the number of copies of probes of the population is dependant on the anticipated abundance of the target in a sample.

The Office, however, points to Fig. 1 and asserts that "each of the population of probes are immobilized onto the membrane in 3 different concentrations 15, 75 and 375 pmol where the WT is expected to be present i.e. *in greater abundance than the other targets.*"

The Applicants disagree and contend that Albitar at FIG. 1 does not teach that the "WT is expected to be present [in the sample] *in greater abundance than the other targets.*" Further, even if the WT (Wild-Type) was expected to be present in the sample in greater abundance than the other targets, there is no teaching that the concentration of the probe populations was in any way affected by that expectation. Rather, all the probes, e.g., mutant and WT, are attached uniformly at the three disclosed density levels. Specifically, Albitar discloses that the WT probes are attached to the membrane in the same concentrations as that of the other mutant probes, regardless of the expected greater abundance of WT target in the sample. Thus, the Applicants contend that because all the probes are attached to the membrane in the same, uniform concentrations, the density of the probes (WT or otherwise) is not dependent upon the anticipated abundance of target in the sample. In fact, disclosing that all the probes for WT or mutant targets are represented at the

same three densities indicates that the number of probe copies is not based on the expected abundance of a given target.

Additionally, Claims 13 and 14 are further distinguished in that they both include the element that the first target is suspected of being present in a higher abundance than that of the second target and thus the number of probe copies and/or density of the populations will vary accordingly. Albitar is completely silent in this regard and, as described above, appears to indicate that the number of probe copies is not based on the expected abundance of a given target, let alone a difference in expected abundance between different targets.

Further, with respect to Claims 15 and 16, these claims are directed to a method of preparing a biopolymeric array. An element of these claims is determining the relative abundance of targets in a sample type for which the array is designed to be used. Nowhere does Albitar teach or suggest this element. Specifically, Albitar is completely silent with respect to the step of determining the relative abundance of targets in a sample type. Albitar is silent in this regard because Albitar is directed to simplifying an assay for determining mutations in the ras gene family and the step of determining the relative abundance of targets in a sample type would unnecessarily add complexity and time to the simplified procedures disclosed in Albitar.

Hence, the Applicants contend that Albitar is deficient in that it fails to teach all the elements of the rejected claims. Specifically, Albitar fails to teach that the number of copies of the population is dependant on the anticipated abundance of the target in a sample and, with respect to Claims 15 and 16, the step of determining the relative abundance of targets in a sample type for which an array is designed to be used. Therefore, because Albitar fails to teach all the elements of the rejected claims it fails to anticipate the claimed invention. In light of the above, the Applicants respectfully request that the 35 U.S.C. § 102(b) rejection of Claims 1-16 be withdrawn.

RECEIVED
CENTRAL FAX CENTER

FEB 22 2007

CONCLUSION

Applicants submit that all of the claims are in condition for allowance, which action is requested. If the Examiner finds that a telephone conference would expedite the prosecution of this application, please telephone Bret Field at (650) 833-7770.

The Commissioner is hereby authorized to charge any underpayment of fees associated with this communication, including any necessary fees for extensions of time, or credit any overpayment to Deposit Account No. 50-1078, order number 10031014-1.

Respectfully submitted,

Date: February 22, 2007

By: _____
James S. Nolan
Registration No. 53,393

Date: February 22, 2007

By: _____
James S. Keddie
Registration No. 48,920

AGILENT TECHNOLOGIES, INC.
Legal Department, DL429
Intellectual Property Administration
P.O. Box 7599
Loveland, CO 80537-0599

F:\DOCUMENT\AGIL\149 (10031014-1)\Response to OA of 12-22-06 10031014-1 (AGIL-149).doc